



#6/a

SEQUENCE LISTING

<110> Detmar, Michael J.
Streit, Michael

<120> THROMBOSPONDIN-2 AND USES THEREOF

<130> 10287-051001

<140> 09/536,087

<141> 2000-03-24

<150> 60/127,221

<151> 1999-03-31

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3596

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)... (3541)

<400> 1

caggagctca	gctgcaggag	gcagg	atg	gtc	tgg	agg	ctg	gtc	ctg	ctg	gct	52
			Met	Val	Trp	Arg	Leu	Val	Leu	Leu	Ala	
			1				5					

ctg	tgg	gtg	tgg	ccc	agc	acg	caa	gct	ggg	cac	cag	gac	aaa	gac	acg	100
Leu	Trp	Val	Trp	Pro	Ser	Thr	Gln	Ala	Gly	His	Gln	Asp	Lys	Asp	Thr	
10				15					20					25		

acc	ttc	gac	ctt	ttc	agt	atc	agc	aac	atc	aac	cgc	aag	acc	att	ggc	148
Thr	Phe	Asp	Leu	Phe	Ser	Ile	Ser	Asn	Ile	Asn	Arg	Lys	Thr	Ile	Gly	
			30					35					40			

gcc	aag	cag	ttc	cgc	ggg	ccc	gac	ccc	ggc	gtg	ccg	gct	tac	cgc	ttc	196
Ala	Lys	Gln	Phe	Arg	Gly	Pro	Asp	Pro	Gly	Val	Pro	Ala	Tyr	Arg	Phe	
		45					50						55			

gtg	cgc	ttt	gac	tac	atc	cca	ccg	gtg	aac	gca	gat	gac	ctc	agc	aag	244
Val	Arg	Phe	Asp	Tyr	Ile	Pro	Pro	Val	Asn	Ala	Asp	Asp	Leu	Ser	Lys	
	60					65				70						

atc	acc	aag	atc	atg	cgg	cag	aag	gag	ggc	ttc	ttc	ctc	acg	gcc	cag	292
Ile	Thr	Lys	Ile	Met	Arg	Gln	Lys	Glu	Gly	Phe	Phe	Leu	Thr	Ala	Gln	
	75					80				85						

ctc	aag	cag	gac	ggc	aag	tcc	agg	ggc	acg	ctg	ttg	gct	ctg	gag	ggc	340
Leu	Lys	Gln	Asp	Gly	Lys	Ser	Arg	Gly	Thr	Leu	Leu	Ala	Leu	Glu	Gly	
	90				95				100						105	

ccc ggt ctc tcc cag agg cag ttc gag atc gtc tcc aat ggc ccc gcg	388
Pro Gly Leu Ser Gln Arg Gln Phe Glu Ile Val Ser Asn Gly Pro Ala	
110 115 120	
gac acg ctg gat ctc acc tac tgg att gac ggc acc cgg cat gtg gtc	436
Asp Thr Leu Asp Leu Thr Tyr Trp Ile Asp Gly Thr Arg His Val Val	
125 130 135	
tcc ctg gag gac gtc ggc ctg gct gac tcg cag tgg aag aac gtc acc	484
Ser Leu Glu Asp Val Gly Leu Ala Asp Ser Gln Trp Lys Asn Val Thr	
140 145 150	
gtg cag gtg gct ggc gag acc tac agc ttg cac gtg ggc tgc gac ctc	532
Val Gln Val Ala Gly Glu Thr Tyr Ser Leu His Val Gly Cys Asp Leu	
155 160 165	
ata gac agc ttc gct ctg gac gag ccc ttc tac gag cac ctg cag gcg	580
Ile Asp Ser Phe Ala Leu Asp Glu Pro Phe Tyr Glu His Leu Gln Ala	
170 175 180 185	
gaa aag agc cgg atg tac gtg gcc aaa ggc tct gcc aga gag agt cac	628
Glu Lys Ser Arg Met Tyr Val Ala Lys Gly Ser Ala Arg Glu Ser His	
190 195 200	
ttc agg ggt ttg ctt cag aac gtc cac cta gtg ttt gaa aac tct gtg	676
Phe Arg Gly Leu Leu Gln Asn Val His Leu Val Phe Glu Asn Ser Val	
205 210 215	
gaa gat att cta agc aag aag ggt tgc cag caa ggc cag gga gct gag	724
Glu Asp Ile Leu Ser Lys Lys Gly Cys Gln Gln Gly Gln Gly Ala Glu	
220 225 230	
atc aac gcc atc agt gag aac aca gag acg ctg cgc ctg ggt ccg cat	772
Ile Asn Ala Ile Ser Glu Asn Thr Glu Thr Leu Arg Leu Gly Pro His	
235 240 245	
gtc acc acc gag tac gtg ggc ccc agc tca gag agg agg ccc gag gtg	820
Val Thr Thr Glu Tyr Val Gly Pro Ser Ser Glu Arg Arg Pro Glu Val	
250 255 260 265	
tgc gaa cgc tcg tgc gag gag ctg gga aac atg gtc cag gag ctc tcg	868
Cys Glu Arg Ser Cys Glu Glu Leu Gly Asn Met Val Gln Glu Leu Ser	
270 275 280	
ggg ctc cac gtc ctc gtg aac cag ccc agc gag aac ctc aag aga gtg	916
Gly Leu His Val Leu Val Asn Gln Pro Ser Glu Asn Leu Lys Arg Val	
285 290 295	
tcg aat gat aac cag ttt ctc tgg gag ctc att ggt ggc cct cct aag	964
Ser Asn Asp Asn Gln Phe Leu Trp Glu Leu Ile Gly Gly Pro Pro Lys	
300 305 310	
aca agg aac atg tca gct tgc tgg cag gat ggc cgg ttc ttt gcg gaa	1012
Thr Arg Asn Met Ser Ala Cys Trp Gln Asp Gly Arg Phe Phe Ala Glu	
315 320 325	

aat gaa acg tgg gtg gtg gac agc tgc acc acg tgt acc tgc aag aaa	1060
Asn Glu Thr Trp Val Val Asp Ser Cys Thr Thr Cys Thr Cys Lys Lys	
330 335 340 345	
ttt aaa acc att tgc cac caa atc acc tgc ccg cct gca acc tgc gcc	1108
Phe Lys Thr Ile Cys His Gln Ile Thr Cys Pro Pro Ala Thr Cys Ala	
350 355 360	
agt cca tcc ttt gtg gaa ggc gaa tgc tgc cct tcc tgc ctc cac tcg	1156
Ser Pro Ser Phe Val Glu Gly Glu Cys Cys Pro Ser Cys Leu His Ser	
365 370 375	
gtg gac ggt gag gag ggc tgg tct ccg tgg gca gag tgg acc cag tgc	1204
Val Asp Gly Glu Glu Gly Trp Ser Pro Trp Ala Glu Trp Thr Gln Cys	
380 385 390	
tcc gtg acg tgt ggc tct ggg acc cag cag aga ggc cgg tcc tgt gac	1252
Ser Val Thr Cys Gly Ser Gly Thr Gln Gln Arg Gly Arg Ser Cys Asp	
395 400 405	
gtc acc agc aac acc tgc ttg ggg ccc tcc atc cag aca cgg gct tgc	1300
Val Thr Ser Asn Thr Cys Leu Gly Pro Ser Ile Gln Thr Arg Ala Cys	
410 415 420 425	
agt ctg agc aag tgt gac acc cgc atc cgg cag gac ggc ggc tgg agc	1348
Ser Leu Ser Lys Cys Asp Thr Arg Ile Arg Gln Asp Gly Gly Trp Ser	
430 435 440	
cac tgg tca cct tgg tct tca tgc tct gtg acc tgt gga gtt ggc aat	1396
His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr Cys Gly Val Gly Asn	
445 450 455	
atc aca cgc atc cgt ctc tgc aac tcc cca gtg ccc cag atg ggg ggc	1444
Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Val Pro Gln Met Gly Gly	
460 465 470	
aag aat tgc aaa ggg agt ggc cgg gag acc aaa gcc tgc cag ggc gcc	1492
Lys Asn Cys Lys Gly Ser Gly Arg Glu Thr Lys Ala Cys Gln Gly Ala	
475 480 485	
cca tgc cca atc gat ggc cgc tgg agc ccc tgg tcc ccg tgg tcg gcc	1540
Pro Cys Pro Ile Asp Gly Arg Trp Ser Pro Trp Ser Pro Trp Ser Ala	
490 495 500 505	
tgc act gtc acc tgt gcc ggt ggg atc cgg gag cgc acc cgg gtc tgc	1588
Cys Thr Val Thr Cys Ala Gly Gly Ile Arg Glu Arg Thr Arg Val Cys	
510 515 520	
aac agc cct gag cct cag tac gga ggg aag gcc tgc gtg ggg gat gtg	1636
Asn Ser Pro Glu Pro Gln Tyr Gly Gly Lys Ala Cys Val Gly Asp Val	
525 530 535	
cag gag cgt cag atg tgc aac aag agg agc tgc ccc gtg gat ggc tgt	1684
Gln Glu Arg Gln Met Cys Asn Lys Arg Ser Cys Pro Val Asp Gly Cys	
540 545 550	
tta tcc aac ccc tgc ttc ccg gga gcc cag tgc agc agc ttc ccc gat	1732

Leu	Ser	Asn	Pro	Cys	Phe	Pro	Gly	Ala	Gln	Cys	Ser	Ser	Phe	Pro	Asp	
555						560					565					
ggg	tcc	tgg	tca	tgc	ggc	tcc	tgc	cct	gtg	ggc	ttc	ttg	ggc	aat	ggc	1780
Gly	Ser	Trp	Ser	Cys	Gly	Ser	Cys	Pro	Val	Gly	Phe	Leu	Gly	Asn	Gly	
570					575					580					585	
acc	cac	tgt	gag	gac	ctg	gac	gag	tgt	gcc	ctg	gtc	ccc	gac	atc	tgc	1828
Thr	His	Cys	Glu	Asp	Leu	Asp	Glu	Cys	Ala	Leu	Val	Pro	Asp	Ile	Cys	
				590					595					600		
ttc	tcc	acc	agc	aag	gtg	cct	cgc	tgt	gtc	aac	act	cag	cct	ggc	ttc	1876
Phe	Ser	Thr	Ser	Lys	Val	Pro	Arg	Cys	Val	Asn	Thr	Gln	Pro	Gly	Phe	
			605					610					615			
cac	tgc	ctg	ccc	tgc	ccg	ccc	cga	tac	aga	ggg	aac	cag	ccc	gtc	ggg	1924
His	Cys	Leu	Pro	Cys	Pro	Pro	Arg	Tyr	Arg	Gly	Asn	Gln	Pro	Val	Gly	
		620					625					630				
gtc	ggc	ctg	gaa	gca	gcc	aag	acg	gaa	aag	caa	gtg	tgt	gag	ccc	gaa	1972
Val	Gly	Leu	Glu	Ala	Ala	Lys	Thr	Glu	Lys	Gln	Val	Cys	Glu	Pro	Glu	
	635					640					645					
aac	cca	tgc	aag	gac	aag	aca	cac	aac	tgc	cac	aag	cac	gcg	gag	tgc	2020
Asn	Pro	Cys	Lys	Asp	Lys	Thr	His	Asn	Cys	His	Lys	His	Ala	Glu	Cys	
650					655					660					665	
atc	tac	ctg	ggc	cac	ttc	agc	gac	ccc	atg	tac	aag	tgc	gag	tgc	cag	2068
Ile	Tyr	Leu	Gly	His	Phe	Ser	Asp	Pro	Met	Tyr	Lys	Cys	Glu	Cys	Gln	
				670					675					680		
aca	ggc	tac	gcg	ggc	gac	ggg	ctc	atc	tgc	ggg	gag	gac	tcg	gac	ctg	2116
Thr	Gly	Tyr	Ala	Gly	Asp	Gly	Leu	Ile	Cys	Gly	Glu	Asp	Ser	Asp	Leu	
			685					690					695			
gac	ggc	tgg	ccc	aac	ctc	aat	ctg	gtc	tgc	gcc	acc	aac	gcc	acc	tac	2164
Asp	Gly	Trp	Pro	Asn	Leu	Asn	Leu	Val	Cys	Ala	Thr	Asn	Ala	Thr	Tyr	
		700					705					710				
cac	tgc	atc	aag	gat	aac	tgc	ccc	cat	ctg	cca	aat	tct	ggg	cag	gaa	2212
His	Cys	Ile	Lys	Asp	Asn	Cys	Pro	His	Leu	Pro	Asn	Ser	Gly	Gln	Glu	
	715					720					725					
gac	ttt	gac	aag	gac	ggg	att	ggc	gat	gcc	tgt	gat	gat	gac	gat	gac	2260
Asp	Phe	Asp	Lys	Asp	Gly	Ile	Gly	Asp	Ala	Cys	Asp	Asp	Asp	Asp	Asp	
730					735					740					745	
aat	gac	ggt	gtg	acc	gat	gag	aag	gac	aac	tgc	cag	ctc	ctc	ttc	aat	2308
Asn	Asp	Gly	Val	Thr	Asp	Glu	Lys	Asp	Asn	Cys	Gln	Leu	Leu	Phe	Asn	
				750					755					760		
ccc	cgc	cag	gct	gac	tat	gac	aag	gat	gag	gtt	ggg	gac	cgc	tgt	gac	2356
Pro	Arg	Gln	Ala	Asp	Tyr	Asp	Lys	Asp	Glu	Val	Gly	Asp	Arg	Cys	Asp	
			765					770					775			
aac	tgc	cct	tac	gtg	cac	aac	cct	gcc	cag	atc	gac	aca	gac	aac	aat	2404
Asn	Cys	Pro	Tyr	Val	His	Asn	Pro	Ala	Gln	Ile	Asp	Thr	Asp	Asn	Asn	

780	785	790	
gga gag ggt gac gcc tgc tcc gtg gac att gat ggg gac gat gtc ttc Gly Glu Gly Asp Ala Cys Ser Val Asp Ile Asp Gly Asp Asp Val Phe 795 800 805			2452
aat gaa cga gac aat tgt ccc tac gtc tac aac act gac cag agg gac Asn Glu Arg Asp Asn Cys Pro Tyr Val Tyr Asn Thr Asp Gln Arg Asp 810 815 820 825			2500
acg gat ggt gac ggt gtg ggg gat cac tgt gac aac tgc ccc ctg gtg Thr Asp Gly Asp Gly Val Gly Asp His Cys Asp Asn Cys Pro Leu Val 830 835 840			2548
cac aac cct gac cag acc gac gtg gac aat gac ctt gtt ggg gac cag His Asn Pro Asp Gln Thr Asp Val Asp Asn Asp Leu Val Gly Asp Gln 845 850 855			2596
tgt gac aac aac gag gac ata gat gac gac ggc cac cag aac aac cag Cys Asp Asn Asn Glu Asp Ile Asp Asp Asp Gly His Gln Asn Asn Gln 860 865 870			2644
gac aac tgc ccc tac atc tcc aac gcc aac cag gct gac cat gac aga Asp Asn Cys Pro Tyr Ile Ser Asn Ala Asn Gln Ala Asp His Asp Arg 875 880 885			2692
gac ggc cag ggc gac gcc tgt gac cct gat gat gac aac gat ggc gtc Asp Gly Gln Gly Asp Ala Cys Asp Pro Asp Asp Asp Asn Asp Gly Val 890 895 900 905			2740
ccc gat gac agg gac aac tgc cgg ctt gtg ttc aac cca gac cag gag Pro Asp Asp Arg Asp Asn Cys Arg Leu Val Phe Asn Pro Asp Gln Glu 910 915 920			2788
gac ttg gac ggt gat gga cgg ggt gat att tgt aaa gat gat ttt gac Asp Leu Asp Gly Asp Gly Arg Gly Asp Ile Cys Lys Asp Asp Phe Asp 925 930 935			2836
aat gac aac atc cca gat att gat gat gtg tgt cct gaa aac aat gcc Asn Asp Asn Ile Pro Asp Ile Asp Asp Val Cys Pro Glu Asn Asn Ala 940 945 950			2884
atc agt gag aca gac ttc agg aac ttc cag atg gtc ccc ttg gat ccc Ile Ser Glu Thr Asp Phe Arg Asn Phe Gln Met Val Pro Leu Asp Pro 955 960 965			2932
aaa ggg acc acc caa att gat ccc aac tgg gtc att cgc cat caa ggc Lys Gly Thr Thr Gln Ile Asp Pro Asn Trp Val Ile Arg His Gln Gly 970 975 980 985			2980
aag gag ctg gtt cag aca gcc aac tcg gac ccc ggc atc gct gta ggt Lys Glu Leu Val Gln Thr Ala Asn Ser Asp Pro Gly Ile Ala Val Gly 990 995 1000			3028
ttt gac gag ttt ggg tct gtg gac ttc agt ggc aca ttc tac gta aac Phe Asp Glu Phe Gly Ser Val Asp Phe Ser Gly Thr Phe Tyr Val Asn 1005 1010 1015			3076

act gac cgg gac gac gac tat gcc ggc ttc gtc ttt ggt tac cag tca 3124
 Thr Asp Arg Asp Asp Asp Tyr Ala Gly Phe Val Phe Gly Tyr Gln Ser
 1020 1025 1030

agc agc cgc ttc tat gtg gtg atg tgg aag cag gtg acg cag acc tac 3172
 Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln Val Thr Gln Thr Tyr
 1035 1040 1045

tgg gag gac cag ccc acg cgg gcc tat ggc tac tcc ggc gtg tcc ctc 3220
 Trp Glu Asp Gln Pro Thr Arg Ala Tyr Gly Tyr Ser Gly Val Ser Leu
 1050 1055 1060 1065

aag gtg gtg aac tcc acc acg ggg acg ggc gag cac ctg agg aac gcg 3268
 Lys Val Val Asn Ser Thr Thr Gly Thr Gly Glu His Leu Arg Asn Ala
 1070 1075 1080

ctg tgg cac acg ggg aac acg ccg ggg cag gtg cga acc tta tgg cac 3316
 Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val Arg Thr Leu Trp His
 1085 1090 1095

gac ccc agg aac att ggc tgg aag gac tac acg gcc tat agg tgg cac 3364
 Asp Pro Arg Asn Ile Gly Trp Lys Asp Tyr Thr Ala Tyr Arg Trp His
 1100 1105 1110

ctg act cac agg ccc aag acc ggc tac atc aga gtc tta gtg cat gaa 3412
 Leu Thr His Arg Pro Lys Thr Gly Tyr Ile Arg Val Leu Val His Glu
 1115 1120 1125

gga aaa cag gtc atg gca gac tca gga cct atc tat gac caa acc tac 3460
 Gly Lys Gln Val Met Ala Asp Ser Gly Pro Ile Tyr Asp Gln Thr Tyr
 1130 1135 1140 1145

gct ggc ggg cgg ctg ggt cta ttt gtc ttc tct caa gaa atg gtc tat 3508
 Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser Gln Glu Met Val Tyr
 1150 1155 1160

ttc tca gac ctc aag tac gaa tgc aga gat att taaacaagat ttgctgcatt 3561
 Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Ile
 1165 1170

tccggcaatg ccctgtgcat gccatggtcc ctaga 3596

<210> 2

<211> 1172

<212> PRT

<213> Homo sapiens

<400> 2

Met Val Trp Arg Leu Val Leu Leu Ala Leu Trp Val Trp Pro Ser Thr
 1 5 10 15
 Gln Ala Gly His Gln Asp Lys Asp Thr Thr Phe Asp Leu Phe Ser Ile
 20 25 30
 Ser Asn Ile Asn Arg Lys Thr Ile Gly Ala Lys Gln Phe Arg Gly Pro
 35 40 45
 Asp Pro Gly Val Pro Ala Tyr Arg Phe Val Arg Phe Asp Tyr Ile Pro
 50 55 60

Pro	Val	Asn	Ala	Asp	Asp	Leu	Ser	Lys	Ile	Thr	Lys	Ile	Met	Arg	Gln	65	70	75	80
Lys	Glu	Gly	Phe	Phe	Leu	Thr	Ala	Gln	Leu	Lys	Gln	Asp	Gly	Lys	Ser	85	90	95	
Arg	Gly	Thr	Leu	Leu	Ala	Leu	Glu	Gly	Pro	Gly	Leu	Ser	Gln	Arg	Gln	100	105	110	
Phe	Glu	Ile	Val	Ser	Asn	Gly	Pro	Ala	Asp	Thr	Leu	Asp	Leu	Thr	Tyr	115	120	125	
Trp	Ile	Asp	Gly	Thr	Arg	His	Val	Val	Ser	Leu	Glu	Asp	Val	Gly	Leu	130	135	140	
Ala	Asp	Ser	Gln	Trp	Lys	Asn	Val	Thr	Val	Gln	Val	Ala	Gly	Glu	Thr	145	150	155	160
Tyr	Ser	Leu	His	Val	Gly	Cys	Asp	Leu	Ile	Asp	Ser	Phe	Ala	Leu	Asp	165	170	175	
Glu	Pro	Phe	Tyr	Glu	His	Leu	Gln	Ala	Glu	Lys	Ser	Arg	Met	Tyr	Val	180	185	190	
Ala	Lys	Gly	Ser	Ala	Arg	Glu	Ser	His	Phe	Arg	Gly	Leu	Leu	Gln	Asn	195	200	205	
Val	His	Leu	Val	Phe	Glu	Asn	Ser	Val	Glu	Asp	Ile	Leu	Ser	Lys	Lys	210	215	220	
Gly	Cys	Gln	Gln	Gly	Gln	Gly	Ala	Glu	Ile	Asn	Ala	Ile	Ser	Glu	Asn	225	230	235	240
Thr	Glu	Thr	Leu	Arg	Leu	Gly	Pro	His	Val	Thr	Thr	Glu	Tyr	Val	Gly	245	250	255	
Pro	Ser	Ser	Glu	Arg	Arg	Pro	Glu	Val	Cys	Glu	Arg	Ser	Cys	Glu	Glu	260	265	270	
Leu	Gly	Asn	Met	Val	Gln	Glu	Leu	Ser	Gly	Leu	His	Val	Leu	Val	Asn	275	280	285	
Gln	Pro	Ser	Glu	Asn	Leu	Lys	Arg	Val	Ser	Asn	Asp	Asn	Gln	Phe	Leu	290	295	300	
Trp	Glu	Leu	Ile	Gly	Gly	Pro	Pro	Lys	Thr	Arg	Asn	Met	Ser	Ala	Cys	305	310	315	320
Trp	Gln	Asp	Gly	Arg	Phe	Phe	Ala	Glu	Asn	Glu	Thr	Trp	Val	Val	Asp	325	330	335	
Ser	Cys	Thr	Thr	Cys	Thr	Cys	Lys	Lys	Phe	Lys	Thr	Ile	Cys	His	Gln	340	345	350	
Ile	Thr	Cys	Pro	Pro	Ala	Thr	Cys	Ala	Ser	Pro	Ser	Phe	Val	Glu	Gly	355	360	365	
Glu	Cys	Cys	Pro	Ser	Cys	Leu	His	Ser	Val	Asp	Gly	Glu	Glu	Gly	Trp	370	375	380	
Ser	Pro	Trp	Ala	Glu	Trp	Gln	Cys	Ser	Val	Thr	Cys	Gly	Ser	Gly		385	390	395	400
Thr	Gln	Gln	Arg	Gly	Arg	Ser	Cys	Asp	Val	Thr	Ser	Asn	Thr	Cys	Leu	405	410	415	
Gly	Pro	Ser	Ile	Gln	Thr	Arg	Ala	Cys	Ser	Leu	Ser	Lys	Cys	Asp	Thr	420	425	430	
Arg	Ile	Arg	Gln	Asp	Gly	Gly	Trp	Ser	His	Trp	Ser	Pro	Trp	Ser	Ser	435	440	445	
Cys	Ser	Val	Thr	Cys	Gly	Val	Gly	Asn	Ile	Thr	Arg	Ile	Arg	Leu	Cys	450	455	460	
Asn	Ser	Pro	Val	Pro	Gln	Met	Gly	Gly	Lys	Asn	Cys	Lys	Gly	Ser	Gly	465	470	475	480
Arg	Glu	Thr	Lys	Ala	Cys	Gln	Gly	Ala	Pro	Cys	Pro	Ile	Asp	Gly	Arg	485	490	495	
Trp	Ser	Pro	Trp	Ser	Pro	Trp	Ser	Ala	Cys	Thr	Val	Thr	Cys	Ala	Gly	500	505	510	
Gly	Ile	Arg	Glu	Arg	Thr	Arg	Val	Cys	Asn	Ser	Pro	Glu	Pro	Gln	Tyr				

		515					520					525					
Gly	Gly	Lys	Ala	Cys	Val	Gly	Asp	Val	Gln	Glu	Arg	Gln	Met	Cys	Asn		
	530					535					540						
Lys	Arg	Ser	Cys	Pro	Val	Asp	Gly	Cys	Leu	Ser	Asn	Pro	Cys	Phe	Pro		
545					550					555					560		
Gly	Ala	Gln	Cys	Ser	Phe	Pro	Asp	Gly	Ser	Trp	Ser	Cys	Gly	Ser			
			565					570						575			
Cys	Pro	Val	Gly	Phe	Leu	Gly	Asn	Gly	Thr	His	Cys	Glu	Asp	Leu	Asp		
			580					585					590				
Glu	Cys	Ala	Leu	Val	Pro	Asp	Ile	Cys	Phe	Ser	Thr	Ser	Lys	Val	Pro		
		595				600						605					
Arg	Cys	Val	Asn	Thr	Gln	Pro	Gly	Phe	His	Cys	Leu	Pro	Cys	Pro	Pro		
610					615						620						
Arg	Tyr	Arg	Gly	Asn	Gln	Pro	Val	Gly	Val	Gly	Leu	Glu	Ala	Ala	Lys		
625					630					635					640		
Thr	Glu	Lys	Gln	Val	Cys	Glu	Pro	Glu	Asn	Pro	Cys	Lys	Asp	Lys	Thr		
			645					650						655			
His	Asn	Cys	His	Lys	His	Ala	Glu	Cys	Ile	Tyr	Leu	Gly	His	Phe	Ser		
		660						665					670				
Asp	Pro	Met	Tyr	Lys	Cys	Glu	Cys	Gln	Thr	Gly	Tyr	Ala	Gly	Asp	Gly		
	675					680						685					
Leu	Ile	Cys	Gly	Glu	Asp	Ser	Asp	Leu	Asp	Gly	Trp	Pro	Asn	Leu	Asn		
690					695					700							
Leu	Val	Cys	Ala	Thr	Asn	Ala	Thr	Tyr	His	Cys	Ile	Lys	Asp	Asn	Cys		
705					710					715					720		
Pro	His	Leu	Pro	Asn	Ser	Gly	Gln	Glu	Asp	Phe	Asp	Lys	Asp	Gly	Ile		
			725					730						735			
Gly	Asp	Ala	Cys	Asp	Asp	Asp	Asp	Asp	Asn	Asp	Gly	Val	Thr	Asp	Glu		
		740				745							750				
Lys	Asp	Asn	Cys	Gln	Leu	Leu	Phe	Asn	Pro	Arg	Gln	Ala	Asp	Tyr	Asp		
	755					760						765					
Lys	Asp	Glu	Val	Gly	Asp	Arg	Cys	Asp	Asn	Cys	Pro	Tyr	Val	His	Asn		
	770				775						780						
Pro	Ala	Gln	Ile	Asp	Thr	Asp	Asn	Asn	Gly	Glu	Gly	Asp	Ala	Cys	Ser		
785					790					795					800		
Val	Asp	Ile	Asp	Gly	Asp	Asp	Val	Phe	Asn	Glu	Arg	Asp	Asn	Cys	Pro		
			805					810						815			
Tyr	Val	Tyr	Asn	Thr	Asp	Gln	Arg	Asp	Thr	Asp	Gly	Asp	Gly	Val	Gly		
		820				825							830				
Asp	His	Cys	Asp	Asn	Cys	Pro	Leu	Val	His	Asn	Pro	Asp	Gln	Thr	Asp		
	835					840						845					
Val	Asp	Asn	Asp	Leu	Val	Gly	Asp	Gln	Cys	Asp	Asn	Asn	Glu	Asp	Ile		
	850				855						860						
Asp	Asp	Asp	Gly	His	Gln	Asn	Asn	Gln	Asp	Asn	Cys	Pro	Tyr	Ile	Ser		
865					870					875					880		
Asn	Ala	Asn	Gln	Ala	Asp	His	Asp	Arg	Asp	Gly	Gln	Gly	Asp	Ala	Cys		
			885					890						895			
Asp	Pro	Asp	Asp	Asp	Asn	Asp	Gly	Val	Pro	Asp	Asp	Arg	Asp	Asn	Cys		
		900				905							910				
Arg	Leu	Val	Phe	Asn	Pro	Asp	Gln	Glu	Asp	Leu	Asp	Gly	Asp	Gly	Arg		
		915				920							925				
Gly	Asp	Ile	Cys	Lys	Asp	Asp	Phe	Asp	Asn	Asp	Asn	Ile	Pro	Asp	Ile		
	930				935						940						
Asp	Asp	Val	Cys	Pro	Glu	Asn	Asn	Ala	Ile	Ser	Glu	Thr	Asp	Phe	Arg		
945					950					955					960		
Asn	Phe	Gln	Met	Val	Pro	Leu	Asp	Pro	Lys	Gly	Thr	Thr	Gln	Ile	Asp		
			965					970						975			

Pro Asn Trp Val Ile Arg His Gln Gly Lys Glu Leu Val Gln Thr Ala
 980 985 990
 Asn Ser Asp Pro Gly Ile Ala Val Gly Phe Asp Glu Phe Gly Ser Val
 995 1000 1005
 Asp Phe Ser Gly Thr Phe Tyr Val Asn Thr Asp Arg Asp Asp Asp Tyr
 1010 1015 1020
 Ala Gly Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val
 1025 1030 1035 1040
 Met Trp Lys Gln Val Thr Gln Thr Tyr Trp Glu Asp Gln Pro Thr Arg
 1045 1050 1055
 Ala Tyr Gly Tyr Ser Gly Val Ser Leu Lys Val Val Asn Ser Thr Thr
 1060 1065 1070
 Gly Thr Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr
 1075 1080 1085
 Pro Gly Gln Val Arg Thr Leu Trp His Asp Pro Arg Asn Ile Gly Trp
 1090 1095 1100
 Lys Asp Tyr Thr Ala Tyr Arg Trp His Leu Thr His Arg Pro Lys Thr
 1105 1110 1115 1120
 Gly Tyr Ile Arg Val Leu Val His Glu Gly Lys Gln Val Met Ala Asp
 1125 1130 1135
 Ser Gly Pro Ile Tyr Asp Gln Thr Tyr Ala Gly Gly Arg Leu Gly Leu
 1140 1145 1150
 Phe Val Phe Ser Gln Glu Met Val Tyr Phe Ser Asp Leu Lys Tyr Glu
 1155 1160 1165
 Cys Arg Asp Ile
 1170

<210> 3
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 3
 Asp Lys Asp Thr Thr Phe Asp Leu Phe Ser Ile Ser Asn Ile Asn
 1 5 10 15

<210> 4
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 4
 gaattcagga gctcagctgc aggaggc

27

<210> 5
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 5
 gaattctagg gaccatggca tgcac

25

<210> 6
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetically generated peptide

<400> 6
 Arg Glu Ser His Phe Arg Gly Leu Leu Gln Asn Val His Leu Val Phe
 1 5 10 15

<210> 7
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetically generated peptide

<400> 7
 Pro Ala Thr Cys Ala Asn Pro Ser Phe Val Glu Gly Glu Cys Cys Pro
 1 5 10 15
 Ser Cys

<210> 8
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetically generated peptide

<400> 8
 Phe Ala Glu Asn Glu Thr Trp Val Val Asp Ser Cys Thr Thr Cys Thr
 1 5 10 15
 Cys Lys Lys Phe Lys Thr
 20

<210> 9
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetically generated peptide

<400> 9
 Glu Leu Ile Gly Gly Pro Pro Lys Thr Arg Asn Met Ser Ala Cys
 1 5 10 15

<210> 10
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetically generated peptide

<400> 10

Trp Ser Pro Trp Ala Glu Trp
1 5

<210> 11

<211> 6

<212> PRT

<213> Homo sapiens

<400> 11

Cys Ser Val Thr Val Gly
1 5